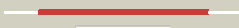


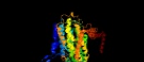

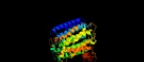

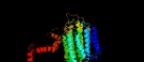

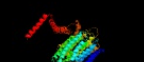

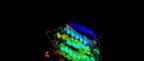

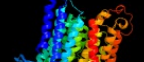

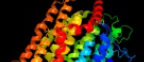



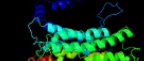

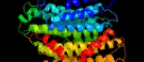
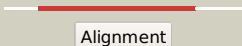



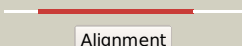

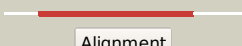

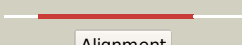
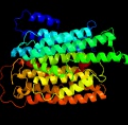
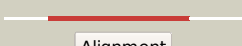








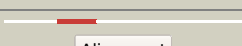
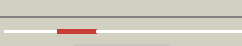
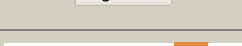
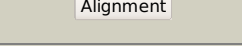
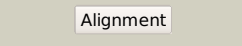
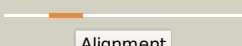



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3156_(nuoL)_3522231_3524132
Date	Thu Aug 8 16:20:34 BST 2019
Unique Job ID	b283e1e8f51caae1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-quinone oxidoreductase subunit l; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c4heaT_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: T: PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
3	c6humF_	 Alignment		100.0	41	PDB header: proton transport Chain: F: PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
4	c6gcs5_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: 5: PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
5	c6g2jL_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
6	c5ldwL_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1
7	c3rkoM_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
8	c6humD_	 Alignment		100.0	19	PDB header: proton transport Chain: D: PDB Molecule: nad(p)h-quinone oxidoreductase chain 4 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
9	c6cfwH_	 Alignment		100.0	24	PDB header: membrane protein Chain: H: PDB Molecule: monovalent cation/h+ antiporter subunit d; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
10	c6gcs4_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: 4: PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
11	c6humB_	 Alignment		100.0	21	PDB header: proton transport Chain: B: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus

12	c4he8M_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
13	c3rkoN_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	c5ldwM_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
15	c4he8I_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh-quinone oxidoreductase subunit 14; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
16	c6gcs2_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: 2: PDB Molecule: nd2 subunit (nu2m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
17	c5xtdi_	 Alignment		100.0	16	PDB header: oxidoreductase/electron transport Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i
18	c6g2jN_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: mouse mitochondrial complex i in the active state
19	c5ldwN_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: structure of mammalian respiratory complex i, class1
20	c6humA_	 Alignment		93.4	14	PDB header: proton transport Chain: A: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
21	c6gcs1_	 Alignment	not modelled	92.7	12	PDB header: oxidoreductase Chain: 1: PDB Molecule: nd1 subunit (nu1m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
22	c5lc5H_	 Alignment	not modelled	91.7	13	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
23	c6cfwM_	 Alignment	not modelled	91.2	7	PDB header: membrane protein Chain: M: PDB Molecule: mbh13 nadh dehydrogenase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
24	c6cfwl_	 Alignment	not modelled	89.3	22	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
25	c3rkoK_	 Alignment	not modelled	88.1	16	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
26	c6humE_	 Alignment	not modelled	87.9	19	PDB header: proton transport Chain: E: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 4i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
27	c6cfwG_	 Alignment	not modelled	82.6	15	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
28	c4heaK_	 Alignment	not modelled	80.1	12	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from

						thermus2 thermophilus
29	c6gcsL_	Alignment	not modelled	78.9	19	PDB header: oxidoreductase Chain: L: PDB Molecule: nd4l subunit (nulum); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
30	d1a6qa1	Alignment	not modelled	36.7	29	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
31	c6g2jK_	Alignment	not modelled	34.3	17	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: mouse mitochondrial complex i in the active state
32	c2kncA_	Alignment	not modelled	30.2	15	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfa-iiib-beta3 transmembrane-cytoplasmic2 heterocomplex
33	d1o8bb1	Alignment	not modelled	28.8	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
34	c2l3ia_	Alignment	not modelled	24.2	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: aoxki4a, antimicrobial peptide in spider venom; PDBTitle: oxi4a, spider derived antimicrobial peptide
35	c4x84C_	Alignment	not modelled	19.9	25	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
36	d1j4na_	Alignment	not modelled	12.8	4	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
37	d1s1qa_	Alignment	not modelled	12.1	31	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
38	c5voxb_	Alignment	not modelled	10.1	13	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
39	d1bcce2	Alignment	not modelled	9.5	26	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
40	c5ldwK_	Alignment	not modelled	9.3	16	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: structure of mammalian respiratory complex i, class1
41	c5lc5K_	Alignment	not modelled	9.3	16	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: structure of mammalian respiratory complex i, class2
42	c5lnkm_	Alignment	not modelled	8.5	30	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
43	d1ppje2	Alignment	not modelled	7.6	26	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
44	c3fq6A_	Alignment	not modelled	7.6	32	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
45	c5zlgA_	Alignment	not modelled	7.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
46	c5ldxb_	Alignment	not modelled	6.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class3.
47	c5o31b_	Alignment	not modelled	6.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
48	c5ldwb_	Alignment	not modelled	6.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class1
49	c5lc5b_	Alignment	not modelled	6.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
50	c4he8H_	Alignment	not modelled	6.5	11	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-quinone oxidoreductase subunit 8; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
51	c5o60M_	Alignment	not modelled	6.5	30	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
52	d3d37a2	Alignment	not modelled	6.3	43	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
53	c6odmK_	Alignment	not modelled	5.8	33	PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
54	c2k1aA_	Alignment	not modelled	5.8	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: bicelle-embedded integrin alpha(iiib) transmembrane segment
						PDB header: membrane protein

55	c4ddpA_	Alignment	not modelled	5.6	27	Chain: A; PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd)
56	c3vp7A_	Alignment	not modelled	5.5	36	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
57	c3j1zP_	Alignment	not modelled	5.4	17	PDB header: metal transport Chain: P; PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy